

SEQUENCE LISTING

<110> Francisco, Joseph  
 McDonagh, Charlotte  
 <120> MODIFIED L49-sFv EXHIBITING INCREASED STABILITY AND METHODS OF USE  
 THEREOF  
 <130> 9632-082-999  
 <140> 10/537,143 (National stage of PCT/US02/38414)  
 <141> 2002-12-02 (371c date)  
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 cag act ctg tcc ctc acc tgt tct gtc act ggc gac tcc atc acc agt 96  
 Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser  
 20 25 30  
 ggt tac tgg aac tgg atc cgg aag ttc cca ggg aat aaa ctt gaa tat 144  
 Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr  
 35 40 45  
 atg ggt tac ata agc gac agt ggt atc act tac tac aat cca tct ctc 192  
 Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu  
 50 55 60  
 aaa agt cgc att tcc atc act cga gac aca tcc aag aac caa tac tac 240  
 Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr  
 65 70 75 80  
 ctc cag ttg aat ttt gtg act gct gag gac aca gcc aca tat aac tgt 288  
 Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys  
 85 90 95  
 gca aga agg act ctg gct act tac tat gct atg gac tac tgg ggt caa 336  
 Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln  
 100 105 110  
 gga acc tct gtc acc gtc tcc tca ggc tcg acg tcc ggc tct ggc aaa 384  
 Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys  
 115 120 125  
 ccg ggc tct ggc gaa ggc tct acc aag ggc gat ttt gtg atg acc caa 432  
 Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln  
 130 135 140  
 act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct 480  
 Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser  
 145 150 155 160  
 tgc agg gct agt cag agc ctt gta cac agt aat gga aac acc tat tta 528  
 Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu  
 165 170 175  
 cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac 576

His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr			
180	185	190	
aga gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt			624
Arg Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser			
195	200	205	
gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag			672
Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu			
210	215	220	
gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt cct ccg acg			720
Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Pro Thr			
225	230	235	240
ttc ggt gga ggc acc aag ctg gaa atc aaa cgg			753
Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg			
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Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr			
35	40	45	
Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu			
50	55	60	
Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr			
65	70	75	80
Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys			
85	90	95	
Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln			
100	105	110	
Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys			
115	120	125	
Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln			
130	135	140	
Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser			
145	150	155	160
Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu			
165	170	175	
His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr			
180	185	190	
Arg Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser			
195	200	205	
Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu			

210

215

220

Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Pro Thr  
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 cag act ctg tcc ctc acc tgt tct gtc act ggc gac tcc atc acc agt 96  
 Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser  
 20 25 30  
 ggt tac tgg aac tgg atc cgg aag ttc cca ggg aat aaa ctt gaa tat 144  
 Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr  
 35 40 45  
 atg ggt tac ata agc gac agt ggt atc act tac aat cca tct ctc 192  
 Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu  
 50 55 60  
 aaa agt cgc att tcc atc act cga gac aca tcc aag aac caa tac tac 240  
 Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr  
 65 70 75 80  
 ctc cag ttg aat ttt gtg act gct gag gac aca gca tat aac tgt 288  
 Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys  
 85 90 95  
 gca aga agg act ctg gct act tac tat gct atg gac tac tgg ggt caa 336  
 Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln  
 100 105 110  
 gga acc tct gtc acc gtc tcc tca ggc tcg acg tcc ggc tct ggc aaa 384  
 Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys  
 115 120 125  
 ccg ggc tct ggc gaa ggc tct acc aag ggc gat ttt gtg atg acc caa 432  
 Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln  
 130 135 140  
 act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct 480  
 Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser  
 145 150 155 160  
 tgc agg gct agt cag agc ctt gta cac agt aat gga aac acc tat tta 528  
 Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu  
 165 170 175  
 cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac 576  
 His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr  
 180 185 190  
 aga gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt 624  
 Arg Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
 195 200 205  
 gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag 672  
 Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu  
 210 215 220  
 gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt cct ccg acg 720

Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Pro Thr			
225 230 235 240			
ttc ggt gga ggc acc aag ctg gaa atc aaa cgg acg cca gtg tca gaa			768
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Pro Val Ser Glu			
245 250 255			
aaa cag ctg gcg gag gtg gtc gcg aat acg att acc ccc ctg atg aaa			816
Lys Gln Leu Ala Glu Val Val Ala Asn Thr Ile Thr Pro Leu Met Lys			
260 265 270			
gcc cag tct gtt cca ggc atg gcg gtg gcc gtt att tat cag gga aaa			864
Ala Gln Ser Val Pro Gly Met Ala Val Ala Val Ile Tyr Gln Gly Lys			
275 280 285			
ccg cac tat tac aca ttt ggc aag gcc gat atc gcg gcg aat aaa ccc			912
Pro His Tyr Tyr Thr Phe Gly Lys Ala Asp Ile Ala Ala Asn Lys Pro			
290 295 300			
gtt acg cct cag acc ctg ttc gag ctg ggt tct ata agt aaa acc ttc			960
Val Thr Pro Gln Thr Leu Phe Glu Leu Gly Ser Ile Ser Lys Thr Phe			
305 310 315 320			
acc ggc gtt tta ggt ggg gat gcc att gct cgc ggt gaa att tcg ctg			1008
Thr Gly Val Leu Gly Gly Asp Ala Ile Ala Arg Gly Glu Ile Ser Leu			
325 330 335			
gac gat gcg gtg acc aga tac tgg cca cag ctg acg ggc aag cag tgg			1056
Asp Asp Ala Val Thr Arg Tyr Trp Pro Gln Leu Thr Gly Lys Gln Trp			
340 345 350			
cag ggt att cgt atg ctg gat ctc gcc acc tac acc gct ggc ggc ctg			1104
Gln Gly Ile Arg Met Leu Asp Leu Ala Thr Tyr Thr Ala Gly Gly Leu			
355 360 365			
ccg cta cag gta ccg gat gag gtc acg gat aac gcc tcc ctg ctg cgc			1152
Pro Leu Gln Val Pro Asp Glu Val Thr Asp Asn Ala Ser Leu Leu Arg			
370 375 380			
ttt tat caa aac tgg cag ccg cag tgg aag cct ggc aca acg cgt ctt			1200
Phe Tyr Gln Asn Trp Gln Pro Gln Trp Lys Pro Gly Thr Thr Arg Leu			
385 390 395 400			
tac gcc aac gcc agc atc ggt ctt ttt ggt gcg ctg gcg gtc aaa cct			1248
Tyr Ala Asn Ala Ser Ile Gly Leu Phe Gly Ala Leu Ala Val Lys Pro			
405 410 415			
tct ggc atg ccc tat gag cag gcc atg acg acg cgg gtc ctt aag ccg			1296
Ser Gly Met Pro Tyr Glu Gln Ala Met Thr Thr Arg Val Leu Lys Pro			
420 425 430			
ctc aag ctg gac cat acc tgg att aac gtg ccg aaa gcg gaa gag gcg			1344
Leu Lys Leu Asp His Thr Trp Ile Asn Val Pro Lys Ala Glu Glu Ala			
435 440 445			
cat tac gcc tgg ggc tat cgt gac ggt aaa gcg gtg cgc gtt tcg ccg			1392
His Tyr Ala Trp Gly Tyr Arg Asp Gly Lys Ala Val Arg Val Ser Pro			
450 455 460			
ggt atg ctg gat gca caa gcc tat ggc gtg aaa acc aac gtg cag gat			1440
Gly Met Leu Asp Ala Gln Ala Tyr Gly Val Lys Thr Asn Val Gln Asp			
465 470 475 480			
atg gcg aac tgg gtc atg gca aac atg gcg ccg gag aac gtt gct gat			1488
Met Ala Asn Trp Val Met Ala Asn Met Ala Pro Glu Asn Val Ala Asp			
485 490 495			
gcc tca ctt aag cag ggc atc gcg ctg gcg cag tcg cgc tac tgg cgt			1536
Ala Ser Leu Lys Gln Gly Ile Ala Leu Ala Gln Ser Arg Tyr Trp Arg			
500 505 510			
atc ggg tca atg tat cag ggt ctg ggc tgg gag atg ctc aac tgg ccc			1584
Ile Gly Ser Met Tyr Gln Gly Leu Gly Trp Glu Met Leu Asn Trp Pro			
515 520 525			
gtg gag gcc aac acg gtg gtc gag acg agt ttt ggt aat gta gca ctg			1632
Val Glu Ala Asn Thr Val Val Glu Thr Ser Phe Gly Asn Val Ala Leu			
530 535 540			
gcg ccg ttg ccc gtg gca gaa gtg aat cca ccg gct ccc ccg gtc aaa			1680
Ala Pro Leu Pro Val Ala Glu Val Asn Pro Pro Ala Pro Pro Val Lys			

545	550	555	560	
gct tcc tgg gtc cat aaa acg ggc tct act ggc ggg ttt ggc agc tac				1728
Ala Ser Trp Val His Lys Thr Gly Ser Thr Gly Gly Phe Gly Ser Tyr				
565	570	575		
gtg gcc ttt att cct gaa aag cag atc ggt att gtg atg ctc gcg aat				1776
Val Ala Phe Ile Pro Glu Lys Gln Ile Gly Ile Val Met Leu Ala Asn				
580	585	590		
aca agc tat ccg aac ccg gca cgc gtt gag gcg gca tac cat atc ctc				1824
Thr Ser Tyr Pro Asn Pro Ala Arg Val Glu Ala Ala Tyr His Ile Leu				
595	600	605		
gag gcg cta cag tag				1839
Glu Ala Leu Gln				
610				
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20	25	30		
Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr				
35	40	45		
Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu				
50	55	60		
Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr				
65	70	75	80	
Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys				
85	90	95		
Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln				
100	105	110		
Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys				
115	120	125		
Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln				
130	135	140		
Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser				
145	150	155	160	
Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu				
165	170	175		
His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr				
180	185	190		
Arg Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser				
195	200	205		
Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu				
210	215	220		

Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Pro Thr  
225 230 235 240

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Pro Val Ser Glu  
245 250 255

Lys Gln Leu Ala Glu Val Val Ala Asn Thr Ile Thr Pro Leu Met Lys  
260 265 270

Ala Gln Ser Val Pro Gly Met Ala Val Ala Val Ile Tyr Gln Gly Lys  
275 280 285

Pro His Tyr Tyr Thr Phe Gly Lys Ala Asp Ile Ala Ala Asn Lys Pro  
290 295 300

Val Thr Pro Gln Thr Leu Phe Glu Leu Gly Ser Ile Ser Lys Thr Phe  
305 310 315 320

Thr Gly Val Leu Gly Gly Asp Ala Ile Ala Arg Gly Glu Ile Ser Leu  
325 330 335

Asp Asp Ala Val Thr Arg Tyr Trp Pro Gln Leu Thr Gly Lys Gln Trp  
340 345 350

Gln Gly Ile Arg Met Leu Asp Leu Ala Thr Tyr Thr Ala Gly Gly Leu  
355 360 365

Pro Leu Gln Val Pro Asp Glu Val Thr Asp Asn Ala Ser Leu Leu Arg  
370 375 380

Phe Tyr Gln Asn Trp Gln Pro Gln Trp Lys Pro Gly Thr Thr Arg Leu  
385 390 395 400

Tyr Ala Asn Ala Ser Ile Gly Leu Phe Gly Ala Leu Ala Val Lys Pro  
405 410 415

Ser Gly Met Pro Tyr Glu Gln Ala Met Thr Thr Arg Val Leu Lys Pro  
420 425 430

Leu Lys Leu Asp His Thr Trp Ile Asn Val Pro Lys Ala Glu Glu Ala  
435 440 445

His Tyr Ala Trp Gly Tyr Arg Asp Gly Lys Ala Val Arg Val Ser Pro  
450 455 460

Gly Met Leu Asp Ala Gln Ala Tyr Gly Val Lys Thr Asn Val Gln Asp  
465 470 475 480

Met Ala Asn Trp Val Met Ala Asn Met Ala Pro Glu Asn Val Ala Asp  
485 490 495

Ala Ser Leu Lys Gln Gly Ile Ala Leu Ala Gln Ser Arg Tyr Trp Arg  
500 505 510

Ile Gly Ser Met Tyr Gln Gly Leu Gly Trp Glu Met Leu Asn Trp Pro  
515 520 525

Val Glu Ala Asn Thr Val Val Glu Thr Ser Phe Gly Asn Val Ala Leu  
530 535 540

Ala Pro Leu Pro Val Ala Glu Val Asn Pro Pro Ala Pro Pro Val Lys  
545 550 555 560

Ala Ser Trp Val His Lys Thr Gly Ser Thr Gly Gly Phe Gly Ser Tyr  
565 570 575

Val Ala Phe Ile Pro Glu Lys Gln Ile Gly Ile Val Met Leu Ala Asn  
580 585 590

Thr Ser Tyr Pro Asn Pro Ala Arg Val Glu Ala Ala Tyr His Ile Leu  
595 600 605

Glu Ala Leu Gln  
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<210> 5  
<211> 27  
<212> DNA  
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<220>  
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<400> 5  
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<210> 6  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Description of Artificial Sequence: Primer

<400> 6  
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<210> 7  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
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<210> 8  
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<212> DNA  
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<210> 9  
<211> 27

<212> DNA  
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<220>  
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<400> 9  
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<210> 10  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Description of Artificial Sequence: Primer

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actggtgatg gagtagccag tgacaga 27

<210> 11  
<211> 27  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 11  
aactggatcc ggcagttccc agggaat 27

<210> 12  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Description of Artificial Sequence: Primer

<400> 12  
attccctggg aactgccgga tccagtt 27

<210> 13  
<211> 33  
<212> DNA  
<213> Artificial

<220>  
<223> Description of Artificial Sequence: Primer

<400> 13  
gggaataaac ttgaatggat gggttacata agc 33

<210> 14  
<211> 33  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

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<210> 15  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Description of Artificial Sequence: Primer

<400> 15  
tccaagaacc aaggctaccc ccagttg 27

<210> 16  
<211> 27  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

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caactggagg taggcttggt tcttgga 27

<210> 17  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Description of Artificial Sequence: Primer

<400> 17  
ctccagttga attctgtgac tgctgag 27

<210> 18  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Description of Artificial Sequence: Primer

<400> 18  
ctcagcagtc acagaattca actggag 27

<210> 19  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Description of Artificial Sequence: Primer

<400> 19  
acagccacat attactgtgc aagaagg 27

<210> 20  
<211> 27  
<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer

<400> 20  
ccttcttgca cagtaatatg tggctgt 27

<210> 21  
<211> 27  
<212> DNA  
<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer

<400> 21  
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<210> 22  
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<223> Description of Artificial Sequence: Primer

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<210> 23  
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<223> Description of Artificial Sequence: Linker Protein

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